

T, 0210

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Luo, Yuling
Xiomei, Xu

(ii) TITLE OF INVENTION: Semaphorin K1 Polypeptides

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
(B) STREET: 75 DENISE DRIVE
(C) CITY: HILLSBOROUGH
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94010

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: OSMAN, RICHARD A
(B) REGISTRATION NUMBER: 36,627
(C) REFERENCE/DOCKET NUMBER: EXEL98-001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 343-4341
(B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2498 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTG CTG CTG CTG CTC TGG GCG GCC GCC GCC TCC GCC CAG GGC CAC CTA
Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu
1 5 10 15

48

21

	AGG AGC GGA CCC CGC ATC TTC GCC GTC TGG AAA GGC CAT GTA GGG CAG	96
	Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln	
	20 25 30	
5	GAC CGG GTG GAC TTT GGC CAG ACT GAG CCG CAC ACG GTG CTT TTC CAC	144
	Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His	
	35 40 45	
	GAG CCA GGC AGC TCC TCT GTG TGG GTG GGA GGA CGT GGC AAG GTC TAC	192
	Glu Pro Gly Ser Ser Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr	
	50 55 60	
10	CTC TTT GAC TTC CCC GAG GGC AAG AAC GCA TCT GTG CGC ACG GTG AAT	240
	Leu Phe Asp Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn	
	65 70 75 80	
	ATC GGC TCC ACA AAG GGG TCC TGT CTG GAT AAG CGG GAC TGC GAG AAC	288
	Ile Gly Ser Thr Lys Gly Ser Cys Leu Asp Lys Arg Asp Cys Glu Asn	
15	85 90 95	
	TAC ATC ACT CTC CTG GAG AGG CGG AGT GAG GGG CTG CTG GCC TGT GGC	336
	Tyr Ile Thr Leu Leu Glu Arg Arg Ser Glu Gly Leu Leu Ala Cys Gly	
	100 105 110	
20	ACC AAC GCC CGG CAC CCC AGC TGC TGG AAC CTG GTG AAT GGC ACT GTG	384
	Thr Asn Ala Arg His Pro Ser Cys Trp Asn Leu Val Asn Gly Thr Val	
	115 120 125	
	GTG CCA CTT GGC GAG ATG AGA GGC TAC GCC CCC TTC AGC CCG GAC GAG	432
	Val Pro Leu Gly Glu Met Arg Gly Tyr Ala Pro Phe Ser Pro Asp Glu	
	130 135 140	
25	AAC TCC CTG GTT CTG TTT GAA GGG GAC GAG GTG TAT TCC ACC ATC CGG	480
	Asn Ser Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg	
	145 150 155 160	
	AAG CAG GAA TAC AAT GGG AAG ATC CCT CGG TTC CGC CGC ATC CGG GGC	528
	Lys Gln Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly	
30	165 170 175	
	GAG AGT GAG CTG TAC ACC AGT GAT ACT GTC ATG CAG AAC CCA CAG TTC	576
	Glu Ser Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe	
	180 185 190	
35	ATC AAA GCC ACC ATC GTG CAC CAA GAC CAG GCT TAC GAT GAC AAG ATC	624
	Ile Lys Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile	
	195 200 205	
	TAC TAC TTC TTC CGA GAG GAC AAT CCT GAC AAG AAT CCT GAG GCT CCT	672
	Tyr Tyr Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro	
	210 215 220	
40	CTC AAT GTG TCC CGT GTG GCC CAG TTG TGC AGG GGG GAC CAG GGT GGG	720
	Leu Asn Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly	
	225 230 235 240	
	GAA AGT TCA CTG TCA GTC TCC AAG TGG AAC ACT TTT CTG AAA GCC ATG	768
	Glu Ser Ser Leu Ser Val Ser Lys Trp Asn Thr Phe Leu Lys Ala Met	

					245					250				255							
					CTG	GTA	TGC	AGT	GAT	GCT	GCC	ACC	AAC	AAG	AAC	TTC	AAC	AGG	CTG	CAA	816
					Leu	Val	Cys	Ser	Asp	Ala	Ala	Thr	Asn	Lys	Asn	Phe	Asn	Arg	Leu	Gln	
										260											
5					GAC	GTC	TTC	CTG	CTC	CCT	GAC	CCC	AGC	GGC	CAG	TGG	AGG	GAC	ACC	AGG	864
					Asp	Val	Phe	Leu	Leu	Pro	Asp	Pro	Ser	Gly	Gln	Trp	Arg	Asp	Thr	Arg	
										275											
					GTC	TAT	GGT	GTT	TTC	TCC	AAC	CCC	TGG	AAC	TAC	TCA	GCC	GTC	TGT	GTG	912
					Val	Tyr	Gly	Val	Phe	Ser	Asn	Pro	Trp	Asn	Tyr	Ser	Ala	Val	Cys	Val	
10																					
										290											
					TAT	TCC	CTC	GGT	GAC	ATT	GAC	AAG	GTC	TTC	CGT	ACC	TCC	TCA	CTC	AAG	960
					Tyr	Ser	Leu	Gly	Asp	Ile	Asp	Lys	Val	Phe	Arg	Thr	Ser	Ser	Leu	Lys	
					305					310					315				320		
					GGC	TAC	CAC	TCA	AGC	CTT	CCC	AAC	CCG	CGG	CCT	GGC	AAG	TGC	CTC	CCA	1008
15					Gly	Tyr	His	Ser	Ser	Leu	Pro	Asn	Pro	Arg	Pro	Gly	Lys	Cys	Leu	Pro	
										325					330				335		
					GAC	CAG	CAG	CCG	ATA	CCC	ACA	GAG	ACC	TTC	CAG	GTG	GCT	GAC	CGT	CAC	1056
					Asp	Gln	Gln	Pro	Ile	Pro	Thr	Glu	Thr	Phe	Gln	Val	Ala	Asp	Arg	His	
										340					345				350		
20					CCA	GAG	GTG	GCG	CAG	AGG	GTG	GAG	CCC	ATG	GGG	CCT	CTG	AAG	ACG	CCA	1104
					Pro	Glu	Val	Ala	Gln	Arg	Val	Glu	Pro	Met	Gly	Pro	Leu	Lys	Thr	Pro	
										355					360				365		
					TTG	TTC	CAC	TCT	AAA	TAC	CAC	TAC	CAG	AAA	GTG	GCC	GTC	CAC	CGC	ATG	1152
					Leu	Phe	His	Ser	Lys	Tyr	His	Tyr	Gln	Lys	Val	Ala	Val	His	Arg	Met	
25																					
										370					375				380		
					CAA	GCC	AGC	CAC	GGG	GAG	ACC	TTT	CAT	GTG	CTT	TAC	CTA	ACT	ACA	GAC	1200
					Gln	Ala	Ser	His	Gly	Glu	Thr	Phe	His	Val	Leu	Tyr	Leu	Thr	Thr	Asp	
					385					390					395				400		
					AGG	GGC	ACT	ATC	CAC	AAG	GTG	GTG	GAA	CCG	GGG	GAG	CAG	GAG	CAC	AGC	1248
30					Arg	Gly	Thr	Ile	His	Lys	Val	Val	Glu	Pro	Gly	Glu	Gln	Glu	His	Ser	
										405					410				415		
					TTC	GCC	TTC	AAC	ATC	ATG	GAG	ATC	CAG	CCC	TTC	CGC	CGC	GCG	GCT	GCC	1296
					Phe	Ala	Phe	Asn	Ile	Met	Glu	Ile	Gln	Pro	Phe	Arg	Arg	Ala	Ala	Ala	
										420					425				430		
35					ATC	CAG	ACC	ATG	TCG	CTG	GAT	GCT	GAG	CGG	AGG	AAG	CTG	TAT	GTG	AGC	1344
					Ile	Gln	Thr	Met	Ser	Leu	Asp	Ala	Glu	Arg	Arg	Lys	Leu	Tyr	Val	Ser	
										435					440				445		
					TCC	CAG	TGG	GAG	GTG	AGC	CAG	GTG	CCC	CTG	GAC	CTG	TGT	GAG	GTC	TAT	1392
					Ser	Gln	Trp	Glu	Val	Ser	Gln	Val	Pro	Leu	Asp	Leu	Cys	Glu	Val	Tyr	
40																					
										450					455				460		
					GGC	GGG	GGC	TGC	CAC	GGT	TGC	CTC	ATG	TCC	CGA	GAC	CCC	TAC	TGC	GGC	1440
					Gly	Gly	Gly	Cys	His	Gly	Cys	Leu	Met	Ser	Arg	Asp	Pro	Tyr	Cys	Gly	
					465					470					475				480		
					TGG	GAC	CAA	GGC	CGC	TGC	ATC	TCC	ATC	TAC	AGC	TCC	GAA	CGG	TCA	GTG	1488

Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val
485 490 495
CTG CAA TCC ATT AAT CCA GCC GAG CCA CAC AAG GAG TGT CCC AAC CCC 1536
Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro
5 500 505 510
AAA CCA GAC AAG GCC CCA CTG CAG AAG GTT TCC CTG GCC CCA AAC TCT 1584
Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser
515 520 525
CGC TAC TAC CTG AGC TGC CCC ATG GAA TCC CGC CAC GCC ACC TAC TCA 1632
10 Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser
530 535 540
TGG CGC CAC AAG GAG AAC GTG GAG CAG AGC TGC GAA CCT GGT CAC CAG 1680
Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln
545 550 555 560
15 AGC CCC AAC TGC ATC CTG TTC ATC GAG AAC CTC ACG GCG CAG CAG TAC 1728
Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr
565 570 575
GGC CAC TAC TTC TGC GAG GCC CAG GAG GGC TCC TAC TTC CGC GAG GCT 1776
20 Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala
580 585 590
CAG CAC TGG CAG CTG CTG CCC GAG GAC GGC ATC ATG GCC GAG CAC CTG 1824
Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu
595 600 605
CTG GGT CAT GCC TGT GCC CTG GCC GCC TCC CTC TGG CTG GGG GTG CTG 1872
25 Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu
610 615 620
CCC ACA CTC ACT CTT GGC TTG CTG GTC CAC TAGGGCCTCC CGAGGCTGGG 1922
Pro Thr Leu Thr Leu Gly Leu Leu Val His
625 630
30 CATGCCTCAG GCTTCTGCAG CCCAGGGCAC TAAAACGTCT CACACTCAGA GCCGGCTGGC 1982
CCGGGAGCTC CTTGCCTGCC ATTTTTCCTCA GGGGACAGAA TAACCCAGTG GAGGATGCCA 2042
GGCCTGGAGA CGTCCAGCCG CAGGCGGCTG CTGGGCCCCA GGTGGCGCAC GGATGGTGGG 2102
GGGCTGAGAA TGAGGGCACC GACTGTGAAG CTGGGGCATC GATGACCCAA GACTTTATTT 2162
TTTGGAATAAT ATTTTTCAGA CTCCTCAAAC TTGACTAAAT GCAGCGATGC TCCCAGCCCA 2222
35 AGAGCCCATG GGTGCGGGAG TGGGTTTGGA TAGGAGAGCT GGGATTCCAT CTCGACCCTG 2282
GGGCTGAGGC CTGAGTCCTT TTGGATTCTT GGTACCCACA TTGCCTCCTT CCCCTCCTTT 2342
TTTCAGGGGT GGGTGGTTGG GTTTCCTGAA GACCCAGGGA TACCCTTTGT CCAGCCCTGT 2402
CCTTGGCAGC TCCCTTTTGT GTCCTGGGTC CCACAGGACA GCCGCCTTGC ATGTTTATTG 2462
AAGGATGTTT GCTTTCCGGA CGGAAGGACG GAAAAA 2498

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 634 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 1 5 10 15
Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu
Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln
 20 25 30
Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His
 35 40 45
10 Glu Pro Gly Ser Ser Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr
 50 55 60
Leu Phe Asp Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn
65 70 75 80
Ile Gly Ser Thr Lys Gly Ser Cys Leu Asp Lys Arg Asp Cys Glu Asn
15 85 90 95
Tyr Ile Thr Leu Leu Glu Arg Arg Ser Glu Gly Leu Leu Ala Cys Gly
 100 105 110
Thr Asn Ala Arg His Pro Ser Cys Trp Asn Leu Val Asn Gly Thr Val
 115 120 125
20 Val Pro Leu Gly Glu Met Arg Gly Tyr Ala Pro Phe Ser Pro Asp Glu
 130 135 140
Asn Ser Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg
145 150 155 160
Lys Gln Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly
25 165 170 175
Glu Ser Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe
 180 185 190
Ile Lys Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile
 195 200 205
30 Tyr Tyr Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro
 210 215 220
Leu Asn Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly
225 230 235 240
Glu Ser Ser Leu Ser Val Ser Lys Trp Asn Thr Phe Leu Lys Ala Met
35 245 250 255
Leu Val Cys Ser Asp Ala Ala Thr Asn Lys Asn Phe Asn Arg Leu Gln
 260 265 270
Asp Val Phe Leu Leu Pro Asp Pro Ser Gly Gln Trp Arg Asp Thr Arg
 275 280 285
40 Val Tyr Gly Val Phe Ser Asn Pro Trp Asn Tyr Ser Ala Val Cys Val
 290 295 300
Tyr Ser Leu Gly Asp Ile Asp Lys Val Phe Arg Thr Ser Ser Leu Lys
305 310 315 320
Gly Tyr His Ser Ser Leu Pro Asn Pro Arg Pro Gly Lys Cys Leu Pro

25

325 330 335
 Asp Gln Gln Pro Ile Pro Thr Glu Thr Phe Gln Val Ala Asp Arg His
 340 345 350
 Pro Glu Val Ala Gln Arg Val Glu Pro Met Gly Pro Leu Lys Thr Pro
 355 360 365
 Leu Phe His Ser Lys Tyr His Tyr Gln Lys Val Ala Val His Arg Met
 370 375 380
 Gln Ala Ser His Gly Glu Thr Phe His Val Leu Tyr Leu Thr Thr Asp
 385 390 395 400
 Arg Gly Thr Ile His Lys Val Val Glu Pro Gly Glu Gln Glu His Ser
 405 410 415
 Phe Ala Phe Asn Ile Met Glu Ile Gln Pro Phe Arg Arg Ala Ala Ala
 420 425 430
 Ile Gln Thr Met Ser Leu Asp Ala Glu Arg Arg Lys Leu Tyr Val Ser
 435 440 445
 Ser Gln Trp Glu Val Ser Gln Val Pro Leu Asp Leu Cys Glu Val Tyr
 450 455 460
 Gly Gly Gly Cys His Gly Cys Leu Met Ser Arg Asp Pro Tyr Cys Gly
 465 470 475 480
 Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val
 485 490 495
 Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro
 500 505 510
 Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser
 515 520 525
 Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser
 530 535 540
 Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln
 545 550 555 560
 Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr
 565 570 575
 Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala
 580 585 590
 Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu
 595 600 605
 Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu
 610 615 620
 Pro Thr Leu Thr Leu Gly Leu Leu Val His
 625 630

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1818 base pairs

(B) TYPE: nucleic acid

05041235 "031198

	Ala Met His Arg Pro Gln Phe Val Gln Ala Thr Ala Val His Lys Asn	
	830 835 840	
	GAA TCT TAT GAT GAT AAA ATC TAC TTT TTC TTT CAA GAA AAC AGC CAC	672
5	Glu Ser Tyr Asp Asp Lys Ile Tyr Phe Phe Phe Gln Glu Asn Ser His	
	845 850 855	
	AGT GAC TTC AAA CAG TTT CCA CAT ACT GTA CCT AGA GTG GGG CAG GTG	720
	Ser Asp Phe Lys Gln Phe Pro His Thr Val Pro Arg Val Gly Gln Val	
	860 865 870	
10	TGC TCT AGT GAT CAA GGT GGG GAG AGC TCC CTG TCT GTC TAC AAG TGG	768
	Cys Ser Ser Asp Gln Gly Gly Glu Ser Ser Leu Ser Val Tyr Lys Trp	
	875 880 885 890	
	ACC ACC TTT TTA AAA GCC AGA CTG GCG TGT GTA GAC TAT GAT ACT GGA	816
	Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Val Asp Tyr Asp Thr Gly	
	895 900 905	
15	AGA ATC TAC AAT GAG CTA CAA GAT ATT TTC ATC TGG CAA GCC CCA GAG	864
	Arg Ile Tyr Asn Glu Leu Gln Asp Ile Phe Ile Trp Gln Ala Pro Glu	
	910 915 920	
	AAC AGC TGG GAA GAG ACT CTC ATC TAT GGA CTT TTT TTG AGC CCG TGG	912
	Asn Ser Trp Glu Glu Thr Leu Ile Tyr Gly Leu Phe Leu Ser Pro Trp	
20	925 930 935	
	AAC TTT TCT GCG GTC TGT GTG TTT ACT GTA AAG GAC ATT GAC CAT GTG	960
	Asn Phe Ser Ala Val Cys Val Phe Thr Val Lys Asp Ile Asp His Val	
	940 945 950	
25	TTT AAG ACA TCC AAG TTA AAA AAT TAT CAT CAT AAA CTC CCC ACA CCT	1008
	Phe Lys Thr Ser Lys Leu Lys Asn Tyr His His Lys Leu Pro Thr Pro	
	955 960 965 970	
	AGA CCA GGG CAA TGC ATG AAG AAC CAT CAG CAT GTT CCC ACA GAA ACC	1056
	Arg Pro Gly Gln Cys Met Lys Asn His Gln His Val Pro Thr Glu Thr	
	975 980 985	
30	TTT CAG GTT GCT GAC AGA TAT CCA GAA GTT GCA GAT CCT GTA TAT CAG	1104
	Phe Gln Val Ala Asp Arg Tyr Pro Glu Val Ala Asp Pro Val Tyr Gln	
	990 995 1000	
	AAG AAC AAT GCC ATG TTT CCA ATA ATT CAG TCA AAA TAT ATC TAC ACC	1152
	Lys Asn Asn Ala Met Phe Pro Ile Ile Gln Ser Lys Tyr Ile Tyr Thr	
35	1005 1010 1015	
	AAA CTA CTT GTT TAT AGG GTA GAG TAT GGA GGT GTT TTT TGG GCA ACT	1200
	Lys Leu Leu Val Tyr Arg Val Glu Tyr Gly Gly Val Phe Trp Ala Thr	
	1020 1025 1030	
40	ATT TTT TAC CTC ACT ACC ATC AAA GGG ACT ATT CAT ATA TAT GTG AGG	1248
	Ile Phe Tyr Leu Thr Thr Ile Lys Gly Thr Ile His Ile Tyr Val Arg	
	1035 1040 1045 1050	
	TAT GAA GAT TCC AAC TCT ACA ACA GCT CTC AAC ATT TTA GAG ATA AAT	1296
	Tyr Glu Asp Ser Asn Ser Thr Thr Ala Leu Asn Ile Leu Glu Ile Asn	
	1055 1060 1065	

CCC TTT CAG AAG CCA GCC CCC ATA CAG AAT ATT CTT TTA GAT AAT ACA 1344
 Pro Phe Gln Lys Pro Ala Pro Ile Gln Asn Ile Leu Leu Asp Asn Thr
 1070 1075 1080
 AAT CTA AAG CTT TAT GTA AAT TCA GAG TGG GAG GTG AGT GAG GTG CCA 1392
 Asn Leu Lys Leu Tyr Val Asn Ser Glu Trp Glu Val Ser Glu Val Pro
 1085 1090 1095
 TTA GAC CTA TGT TCA GTG TAT GGG AAT GAT TGT TTC AGC TGT TTT ATG 1440
 Leu Asp Leu Cys Ser Val Tyr Gly Asn Asp Cys Phe Ser Cys Phe Met
 1100 1105 1110
 TCA AGG GAT CCC CTG TGC ACA TGG TAT AAC AAC ACC TGT TCC TTT AAA 1488
 Ser Arg Asp Pro Leu Cys Thr Trp Tyr Asn Asn Thr Cys Ser Phe Lys
 1115 1120 1125 1130
 CAG AGA GTA TCT GTT GAA ACC GGT GGT CCA GCT AAC CGC ACC CTT TCA 1536
 Gln Arg Val Ser Val Glu Thr Gly Gly Pro Ala Asn Arg Thr Leu Ser
 1135 1140 1145
 GAA ATG TGT GGT GAC CAC TAT GCT CCA ACT GTG GTT AAG CAT CAA GTT 1584
 Glu Met Cys Gly Asp His Tyr Ala Pro Thr Val Val Lys His Gln Val
 1150 1155 1160
 TCT ATA CCT CTA TTA TCT AAT TCT TAT TTG TCC TGC CCA GCA GTC TCA 1632
 Ser Ile Pro Leu Leu Ser Asn Ser Tyr Leu Ser Cys Pro Ala Val Ser
 1165 1170 1175
 AAC CAC GCT GAC TAC TTT TGG ACT AAA GAT GGT TTC ACA GAA AAA AGA 1680
 Asn His Ala Asp Tyr Phe Trp Thr Lys Asp Gly Phe Thr Glu Lys Arg
 1180 1185 1190
 TGC CAT GTC AAA ACA CAC AAA AAT GAC TGC ATC TTG CTT ATA GCT AAC 1728
 Cys His Val Lys Thr His Lys Asn Asp Cys Ile Leu Leu Ile Ala Asn
 1195 1200 1205 1210
 AGC ACG ACA GCC ACT AAT GGA ACC CAC GTG TGC AAC ATG AAA GAA GAT 1776
 Ser Thr Thr Ala Thr Asn Gly Thr His Val Cys Asn Met Lys Glu Asp
 1215 1220 1225
 TCG GTG ACA GTG AAA CTG TTA GAG GTG AAT GTG ACA CTG ATG 1818
 Ser Val Thr Val Lys Leu Leu Glu Val Asn Val Thr Leu Met
 1230 1235 1240

35 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 606 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Thr Leu Cys Val Ser Ile Arg Leu Leu Met Ile Leu Ser Ala
 1 5 10 15
 Ile Thr Ala Ala Lys Ser Arg Phe Ile Asp Lys Pro Arg Leu Ile Val

20 25 30
 Asn Leu Thr Asp Gly Phe Gly Gln His Arg Phe Phe Gly Pro Gln Glu
 35 40 45
 5 Pro His Thr Val Leu Phe His Ser Leu Asn Ser Ser Asp Val Tyr Val
 50 55 60
 Gly Gly Asn Asn Thr Ile Tyr Leu Phe Asp Phe Ala His Ser Ser Asn
 65 70 75 80
 Ala Ser Thr Ala Leu Ile Asn Ile Thr Ser Thr His Asn Thr His Arg
 85 90 95
 10 Leu Ser Ser Thr Cys Glu Asn Phe Ile Thr Leu Leu His Asn Gln Thr
 100 105 110
 Asp Gly Leu Leu Ala Cys Gly Thr Asn Ser Gln Lys Pro Ser Cys Trp
 115 120 125
 Leu Ile Asn Asn Leu Thr Thr Gln Phe Leu Gly Pro Lys Leu Gly Leu
 130 135 140
 15 Ala Pro Phe Ser Pro Ser Ser Gly Asn Leu Val Leu Phe Asp Gln Asn
 145 150 155 160
 Asp Thr Tyr Ser Thr Ile Asn Leu Tyr Lys Ser Leu Ser Gly Ser His
 165 170 175
 20 Lys Phe Arg Arg Ile Ala Gly Gln Val Glu Leu Tyr Thr Ser Asp Thr
 180 185 190
 Ala Met His Arg Pro Gln Phe Val Gln Ala Thr Ala Val His Lys Asn
 195 200 205
 Glu Ser Tyr Asp Asp Lys Ile Tyr Phe Phe Phe Gln Glu Asn Ser His
 210 215 220
 25 Ser Asp Phe Lys Gln Phe Pro His Thr Val Pro Arg Val Gly Gln Val
 225 230 235 240
 Cys Ser Ser Asp Gln Gly Gly Glu Ser Ser Leu Ser Val Tyr Lys Trp
 245 250 255
 30 Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Val Asp Tyr Asp Thr Gly
 260 265 270
 Arg Ile Tyr Asn Glu Leu Gln Asp Ile Phe Ile Trp Gln Ala Pro Glu
 275 280 285
 Asn Ser Trp Glu Glu Thr Leu Ile Tyr Gly Leu Phe Leu Ser Pro Trp
 290 295 300
 35 Asn Phe Ser Ala Val Cys Val Phe Thr Val Lys Asp Ile Asp His Val
 305 310 315 320
 Phe Lys Thr Ser Lys Leu Lys Asn Tyr His His Lys Leu Pro Thr Pro
 325 330 335
 40 Arg Pro Gly Gln Cys Met Lys Asn His Gln His Val Pro Thr Glu Thr
 340 345 350
 Phe Gln Val Ala Asp Arg Tyr Pro Glu Val Ala Asp Pro Val Tyr Gln
 355 360 365
 Lys Asn Asn Ala Met Phe Pro Ile Ile Gln Ser Lys Tyr Ile Tyr Thr

09041236-031198

	370		375		380
	Lys Leu Leu Val Tyr Arg	Val Glu Tyr Gly Gly	Val Phe Trp Ala Thr		
	385	390	395	400	
5	Ile Phe Tyr Leu Thr Thr	Ile Lys Gly Thr	Ile His Ile Tyr Val Arg		
	405	410	415		
	Tyr Glu Asp Ser Asn Ser Thr Thr	Ala Leu Asn Ile Leu Glu Ile Asn			
	420	425	430		
	Pro Phe Gln Lys Pro Ala Pro	Ile Gln Asn Ile Leu Leu Asp Asn Thr			
	435	440	445		
10	Asn Leu Lys Leu Tyr Val Asn Ser Glu Trp Glu Val Ser Glu Val Pro				
	450	455	460		
	Leu Asp Leu Cys Ser Val Tyr Gly Asn Asp Cys Phe Ser Cys Phe Met				
	465	470	475	480	
	Ser Arg Asp Pro Leu Cys Thr Trp Tyr Asn Asn Thr Cys Ser Phe Lys				
15	485	490	495		
	Gln Arg Val Ser Val Glu Thr Gly Gly Pro Ala Asn Arg Thr Leu Ser				
	500	505	510		
	Glu Met Cys Gly Asp His Tyr Ala Pro Thr Val Val Lys His Gln Val				
	515	520	525		
20	Ser Ile Pro Leu Leu Ser Asn Ser Tyr Leu Ser Cys Pro Ala Val Ser				
	530	535	540		
	Asn His Ala Asp Tyr Phe Trp Thr Lys Asp Gly Phe Thr Glu Lys Arg				
	545	550	555	560	
	Cys His Val Lys Thr His Lys Asn Asp Cys Ile Leu Leu Ile Ala Asn				
25	565	570	575		
	Ser Thr Thr Ala Thr Asn Gly Thr His Val Cys Asn Met Lys Glu Asp				
	580	585	590		
	Ser Val Thr Val Lys Leu Leu Glu Val Asn Val Thr Leu Met				
	595	600	605		

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